U.S.S.N 09/687,483 Braun *et al.* PRELIMINARY AMENDMENT

## **REMARKS**

Any fees that may be due in connection with this application throughout its pendency may be charged to Deposit Account No. 50-1213.

The specification is amended to add a formula that was inadvertently omitted from the specification as originally filed. In a preliminary amendment filed February 15, 2001, brackets were inadvertently placed in the formula that was sought to be added to the specification. The instant amendment seeks to remove the brackets. Basis for this amendment can be found in the specification, in particular page 108, lines 15-21, which describes a root mean square calculation of the residual error and defines the algebraic terms of the residual error formula. Thus, no new matter has been added.

Included as an attachment is a marked-up version of the specification paragraphs that are being amended, per 37 CFR §1.121.

\* \* \*

Entry of this amendment and examination of the application are respectfully requested.

Respectfully submitted,
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By:

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Serial No.

Braun et al.

09/687,483

Filed:

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For:

METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING POLYMORPHIC GENETIC MARKERS

Art Unit:

1645

Examiner:

Unassigned

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## ATTACHMENT TO THE PRELIMINARY AMENDMENT MARKED UP PARAGRAPHS AND CLAIMS (37 CFR §1.121)

## IN THE SPECIFICATION:

Please amend the specification as follows:

Please amend the paragraph on page 108, lines 15-21, as follows:

Referring to FIG. 51, a residual error is calculated by taking a root mean square calculation between the Gaussian 293 and the putative peak 290 in the data signal. The calculation is performed on data within one width on either side of a center line of the Gaussian. The residual error is calculated as:  $\sqrt{(G-R)^2/N}$ 

where G is the Gaussian signal value, R is the putative peak value, and N is the number of points from -W to +W. The calculated residual error is

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used to generate an adjusted signal-to-noise ratio, as described below.

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